

K. Carlson

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/207,161

#10  
4/13/2008  
DATE: 03/22/2000  
TIME: 11:50:12

INPUT SET: S35114.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

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(1) General Information:

- (i) APPLICANT: Hillman, Jennifer L.  
Goli, Surya K.
- (ii) TITLE OF INVENTION: NOVEL HUMAN INTEGRAL MEMBRANE  
PROTEIN
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/207,161  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US/08/791,338  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0208 US
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

ENTERED

RAW SEQUENCE LISTING  
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## (i) SEQUENCE CHARACTERISTICS:

49

(A) LENGTH: 266 amino acids

50

(B) TYPE: amino acid

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(C) STRANDEDNESS: single

52

(D) TOPOLOGY: linear

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54

## (vii) IMMEDIATE SOURCE:

55

(A) LIBRARY: NEUTGMT01

56

(B) CLONE: 632664

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58

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

59

60

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys

61

1 5 10 15

62

Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp

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20 25 30

64

Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly

65

35 40 45

66

Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met

67

50 55 60

68

Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala

69

65 70 75 80

70

Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp

71

85 90 95

72

Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr

73

100 105 110

74

Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu

75

115 120 125

76

Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn

77

130 135 140

78

Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn

79

145 150 155 160

80

Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro

81

165 170 175

82

Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly Thr Tyr

83

180 185 190

84

Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg

85

195 200 205

86

Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His

87

210 215 220

88

Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile

89

225 230 235 240

90

Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn

91

245 250 255

92

Lys Phe Ala Val Glu Thr Leu Ile Cys Ser

93

260 265

94

95

## (2) INFORMATION FOR SEQ ID NO:2:

96

97

## (i) SEQUENCE CHARACTERISTICS:

98

(A) LENGTH: 1114 base pairs

99

(B) TYPE: nucleic acid

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/207,161

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100      (C) STRANDEDNESS: single
101      (D) TOPOLOGY: linear
102
103      (vii) IMMEDIATE SOURCE:
104          (A) LIBRARY: NEUTGMT01
105          (B) CLONE: 632664
106
107      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
108
109      GCCGCCTCTG CCGCCGCGGA CTTCCCGAAC CTCTTCAGCC GCCCGGAGCC GCTCCCGGAG      60
110      CCCGGCCGTA GAGGCTGCAA TCGCAGCCGG TGAGCCCGCA GCCCGCGCCC CGAGCCCGCC      120
111      CCCGCCCTTC GAGGGCGCCC CAGGCCGCGC CATGGTGAAG GTGACGTTCA ACTCCGCTCT      180
112      GGCCCAGAAG GAGGCCAAGA AGGACGAGCC CAAGAGCGGC GAGGAGGCGC TCATCATCCC      240
113      CCCCAGCGCC GTCGCGGTGG ACTGCAAGGA CCCAGATGAT GTGGTACCAG TTGGCCAAAG      300
114      AAGAGCCTGG TGTGGTGCA TGTGCTTTGG ACTAGCATTT ATGCTTGCAG GTGTTATTCT      360
115      AGGAGGAGCA TACTTGTA CAATATTTTGC ACTTCAACCA GATGACGTGT ACTACTGTGG      420
116      AATAAAGTAC ATCAAAGATG ATGTCATCTT AAATGAGCCC TCTGCAGATG CCCAGCTGTC      480
117      TCTCTACCAG ACAATTGAAG AAAATATTA AATCTTTGAA GAAGAAGAAG TTGAATTTAT      540
118      CAGTGTGCCT GTCCAGAGT TTGCAGATAG TGATCCTGCC AACATTGTTC ATGACTTTAA      600
119      CAAGAACTT ACAGCCTATT TAGATCTTAA CCTGGATAAG TGCTATGTGA TCCCTCTGAA      660
120      CACTTCCATT GTTATGCCAC CCAGAAACCT ACTGGAGTTA CTTATTAACA TCAAGGCTGG      720
121      AACCTATTTG CCTCAGTCCT ATCTGATTCA TGAGCACATG GTTATTACTG ATCGCATTGA      780
122      AAACATTGAT CACCTGGGTT TCTTTATTTA TCGACTGTGT CATGACAAGG AAACCTACAA      840
123      ACTGCAACGC AGAGAAACTA TTAAAGGTAT TCAGAAACGT GAAGCCAGCA ATTGTTTCGC      900
124      AATTCGGCAT TTTGAAAACA AATTTGCCGT GGAAACTTTA ATTTGTTCTT GAACAGTCAA      960
125      GAAAAACATT ATTGAGGAAA ATTAATATCA CAGCATAACC CCACCCTTTA CATTTTGTGC      1020
126      AGTGATTATT TTTTAAAGTC TTCTTTCATG TAAGTAGCAA ACAGGGCTTT ACTATCTTTT      1080
127      CATCTCATTA ATTCAATTAA AACCATTACC TTAA      1114

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(2) INFORMATION FOR SEQ ID NO:3:

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131      (i) SEQUENCE CHARACTERISTICS:
132          (A) LENGTH: 263 amino acids
133          (B) TYPE: amino acid
134          (C) STRANDEDNESS: single
135          (D) TOPOLOGY: linear

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136
137      (vii) IMMEDIATE SOURCE:
138          (A) LIBRARY: GenBank
139          (B) CLONE: 624778

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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141
142
143      Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
144          1           5           10           15
145      Ala Arg Gln Asp Ile Glu Ala Leu Val Ser Arg Thr Val Arg Ala Gln
146          20           25           30
147      Ile Leu Thr Gly Lys Glu Leu Arg Val Val Pro Gln Glu Lys Asp Gly
148          35           40           45
149      Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu
150          50           55           60
151      Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
152          65           70           75           80

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153 Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Glu Asp  
154 85 90 95  
155 Pro Val Asn Ser Ile Pro Gly Gly Glu Pro Tyr Phe Leu Pro Val Thr  
156 100 105 110  
157 Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val  
158 115 120 125  
159 Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp  
160 130 135 140  
161 Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys  
162 145 150 155 160  
163 Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Thr Pro Lys Asn Leu  
164 165 170 175  
165 Val Glu Leu Phe Gly Lys Leu Ala Ser Gly Lys Tyr Leu Pro His Thr  
166 180 185 190  
167 Tyr Val Val Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val  
168 195 200 205  
169 Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser  
170 210 215 220  
171 Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala  
172 225 230 235 240  
173 Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val  
174 245 250 255  
175 Glu Thr Lys Ile Cys Gln Glu  
176 260  
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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1635 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
(B) CLONE: 624777

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

191  
192 GGGAGACCTG AGCTCGCTGC TGCCTGTGGA AGACTGGGAG AGGAGACACT AAGTGCTGCT 60  
193 CAAGCAAGCG CGATCCTCTC CTCTTTCAAC CTGCAGCCCA AGATACTGAT TCGAGCCGCG 120  
194 CCTTACCGCG CAGCCCGAAG ATTCACCATG GTGAAGATCG CCTTCAACAC CCCTACGGCG 180  
195 GTGCAAAAGG AGGAGGCGCG GCAAGATATA GAGGCGCTCG TCAGTCGCAC TGTCCGAGCT 240  
196 CAAATCCTGA CTGGCAAGGA GCTCAGAGTT GTCCCGCAGG AGAAAGATGG CTCATCTGGG 300  
197 AGATGCATGC TTA CTCTCCT AGGCCTCTCA TTCATCTTGG CAGGACTGAT TGTGTTGGTGA 360  
198 GCCTGCATTT ACAAGTACTT CATGCCCAAG AGCACCATTT ACCATGGTGA GATGTGCTTC 420  
199 TTTGATTCTG AGGATCCTGT CAATTCCATT CCTGGAGGAG AGCCATACTT TCTGCCTGTG 480  
200 ACTGAGGAGG CTGATATCCG TGAGGATGAC AACATTGCCA TCATTGATGT GCCTGTGCCC 540  
201 AGTTTCTCTG ATAGCGATCC GGCGGCAATT ATTCACGACT TTGAGAAGGG AATGACTGCT 600  
202 TACCTGGACT TGCTTTTGGG AAAGTGTAT CTGATGCCCC TCAATACTTC CATGTGTTATG 660  
203 ACTCCAAAGA ATCTGGTGGA ACTTTTGGGA AAAGTGGCAA GTGGCAAGTA TTTGCCTCAT 720  
204 ACTTATGTGG TTCGTGAAGA CCTGGTTGCT GTGGAAGAAA TTCGTGATGT TAGTAACCTT 780  
205 GGTATTTTTA TTTACCAACT TTGCAACAAC CGAAAATCCT TCCGCCTTAG ACGCAGAGAC 840

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206	CTTCTGCTGG	GTTTCAACAA	GCGTGCCATT	GACAAATGCT	GGAAGATTAG	ACACTTCCCC	900
207	AATGAATTTA	TCGTTGAAAC	CAAGATCTGT	CAGGAGTGAA	ATGTGACAGA	TAAAGAGTAT	960
208	CCTTGATAAT	AAGAAGTCAG	GAACTTACCG	TCTGACTTGG	AAAATTGAAA	TTGATGGGAT	1020
209	ACTCATGCTA	TTTACTCATA	CATTTACTCT	ATTGCTTATA	CTGGAAAAGG	AAAGGGAAAAG	1080
210	GGGGGAGAAA	ACTACTAACC	ACTGCAAGCG	ATTGTCCAAT	TCTACTTTAA	TTGACATTGC	1140
211	TTGCTGTTTT	CAACAAGTCA	AATGATTATC	TTTTCTCTTG	AATTTATAGG	GTTTAGATTT	1200
212	CTGAAAGCAG	CATGAATGTG	TCATCTTACC	ATCCTGACAA	TAAAGCCCAT	CCTCTGGTTT	1260
213	TATTTAAAGC	AAGCTCTTTC	CAACATCACT	TGGCTAGAGC	ATGCTTTAAA	TTTAAAATAT	1320
214	TTGAAATTTG	TTTTTGACAT	TTTTTTGTGT	GAAACATGTC	AAATCTCTTA	CCATTCTTTG	1380
215	GTTTTCTTCT	TTATTATGTT	CAACTCTCCT	GATTTGAGAA	GTTACATTTT	TGCATTTCTA	1440
216	TCAGGTGCTG	TGTAACGAAT	CTGACTGATA	TGTGAACAAT	CTTCATGAGG	AAGCAATTTT	1500
217	TTACTCATGT	AATGATTCTT	TCTCACTGAT	ATCTGTATTG	TGAAATCCAC	AGAACTGTAC	1560
218	AGGTGCTGAA	TGCTGTAAGG	AGTTCTGGTT	GTATGAATTC	TACAACCCTA	TAATAAAGTT	1620
219	TACCGTATTC	AATCA					1635
220							
221							

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/207,161**

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Original Text